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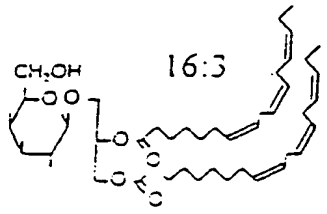

FIGURE 1

A


```
soMGD A    MSHPST/TSEPSN-LLDFVPKLGNFVLNSSLHGNNSNGYSSFSSNSVHFGGLAT----QN  55
csMGD A    MRNPST//QENGS-VSDFISQLGYFAFSSRFLNLNSEGCSGSSSHSLYLNGFENYRCVKP  59
atMGD A    MQNPST//QESAAPVFDFFPRLRGLTSRNRSPCSNSDGYALSSSNALYFNGFRTLPS-RR  59
atMGD B    ------------------------------------------------------------  0

soMGD A    RYKFVNSLSF---SKEGSNLKRILSDFNRVIRLHCDRI-PLGFSSIGLN--SGESNGVSD 109
csMGD A    PPRSGASLSLS--SRGSSSLRRFVNEFNNVIKFHCHKP-PLGFASLGGV--SDETNGIRD 114
atMGD A    MGKTLASLSFNTKSSAGSSLRRFISDFNSFIRFHCDKVVPESPASVGGVGLSSDENGIRE 119
atMGD B    ----MATTVM---ALAEKVLERVVGTSKSAVSVTSGDGEKTHRHTHHHIHRIKSYDDIDE 53

soMGD A    NGHG-VLEDVRVPVNAVEPESPKRVLILMSDTGGGHRASAEAIKAAFNEEFGDDYQVFVT 168
csMGD A    DGFG-VSQDGALPLNKIEAENPKRVLILMSDTGGGHRASAEAIKAAFNEEFGNNYQVFIT 173
atMGD A    NGTGGVLGEEGLPLNGVEADRPKKVLILMSDTGGGHRASAEAIRAAFNQEFGDEYQVFIT 179
atMGD B    DESS-------LELIQIGAERTKNVLILMSDTGGGHRASAEAIRDAFKIEFGDKYRVIVK 106

                                                    h1
soMGD A    DLWSERTPWPFNQLPRSYNFLVKHGPLWKMMYYGTSPRVIHQSNFAATSVFIAREVARGL 228
csMGD A    DLWTDHTPWPFNQLPRSYNFLVKHGTLWKMTYYVTAPKVIHQSNFAATSTFIAREVAKGL 233
atMGD A    DLWTDHTPWPFNQLPRSYNFLVKHGTLWKMTYYGTSPRIVHQSNFAATSTFIAREIAQGL 239
atMGD B    DVWKEYTGWPLNDMERSYKFMVKHVQLWKVAFHSTSPKWIHSCYLAAIAAYYAKEVEAGL 166

                                                        h2*
soMGD A    MKYQPDIIISVHPLMQHVPLRILRGRGLLEKIVFTTVVTDLSTCHPTWFHKLVTRCYCPS 288
csMGD A    MKYRPDIIISVHPLMQHVPIRILRSKGLLNKIVFTTVVTDLSTCHPTWFHKLVTRCYCPS 293
atMGD A    MKYQPDIIISVHPLMQHVPLRVLRSKGLLKKIVFTTVITDLSTCHPTWFHKLVTRCYCPS 299
atMGD B    MEYKPEIIISVHPLMQHIPLWVLKWQELQKRVLFVTVITDLNTCHPTWFHPGVNRCYCPS 226

soMGD A    NEVAKRATKAGLQPSQIKVYGLPVRPSFVRSVRPKNELRKELGMDEHLPAVLLMGGGEGM 348
csMGD A    TEVAKRALTAGLQPSKLKVFGLPVRPSFVKPIRPKIELRKELGMDENLPAVLLMGGGEGM 353
atMGD A    TEVAKRAQKAGLETSQIKVYGLPVRPSFVKPVRPKVELRRELGMDENLPAVLLMGGGEGM 359
atMGD B    QEVAKRALFDGLDESQVRVFGLPVRPSFARAVLVKCDLRKELEMDQDLRAVLLMGGGEGM 286

                h3*                                 h4
soMGD A    GPIEATARALGNALYDANLGEPTGQLLVICGRNKKLAGKLSSIDWKIPVQVKGFVTKIEE 408
csMGD A    GPIEATAKALSKALYDENHGEPIGQVLVICGHNKKLAGRLRSIDWKVPVQVKGFVTKMEE 413
atMGD A    GPIEATARALADALYDKNLGEAVGQVLIICGRNKKLQSKLSSLDWKIPVQVKGFITKMEE 419
atMGD B    GPVKETAKALEEFLYDKENRKPIGQMVVICGRNKKLASALEAIDWKIPVKVRGFETQMEK 346

                h5*
soMGD A    CMGACDCIITKAGPGTIAEAMIRGLPIILNDYIAGQEAGNVPYVIENGIGKYLKSPKEIA 468
csMGD A    CMGACDCIITKAGPGTIAEAMIRGLPIILNDYIAGQEAGNVPYVVENGCGKFSKSPKEIA 473
atMGD A    CMGACDCIITKAGPGTIAEAMIRGLPIILNGYIAGQEAGNVPYVVENGCGKFSKSPKEIS 479
atMGD B    WMGACDCIITKAGPGTIAESLIRSLPIILNDYIPGQEKGNVPYVVENGAGVFTRSPKETA 406

                h6*
soMGD A    KIVSQWFGPKANELQIMSQNALKHARPDAVFKIVHDLDELVRQKIFVRQYSCAA------ 522
csMGD A    NIVAKWFGPKADELLIMSQNALRLARPDAVFKIVHDLHELVKQRSFVPQYSG-------- 525
atMGD A    KIVADWFGPASKELEIMSQNALRLAKPEAVFKIVHDMHELVRKKNSLPQLSCTA------ 533
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                                                    h7*
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B

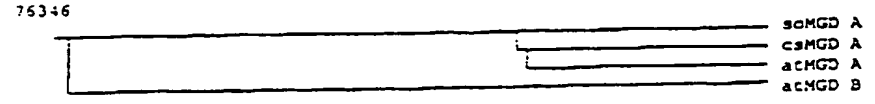
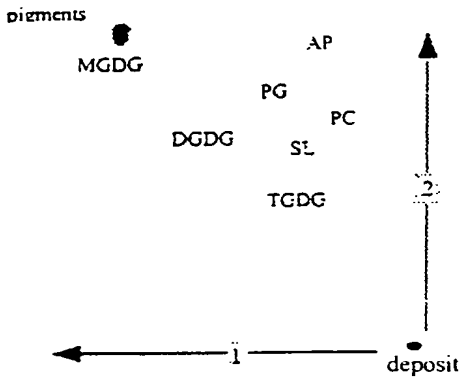


FIGURE 2

A



B

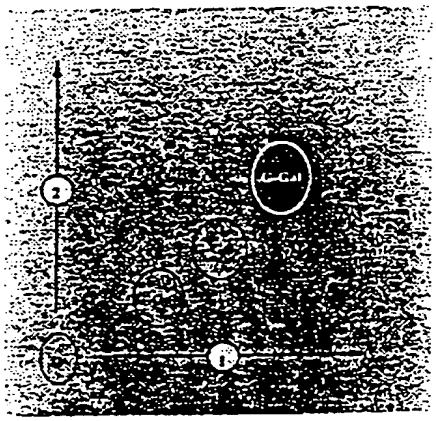


FIGURE 3

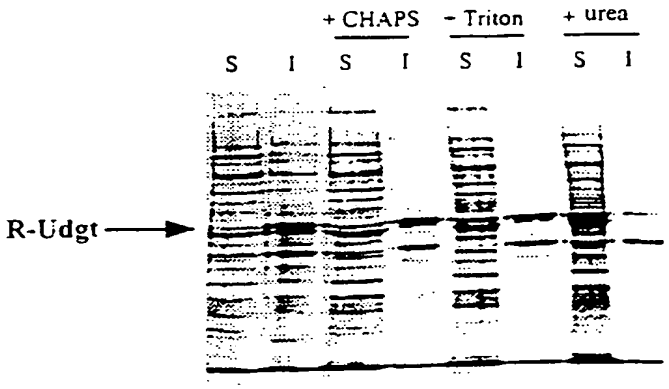


FIGURE 4

DOCKET #1339346127 SHEET 4 OF 5

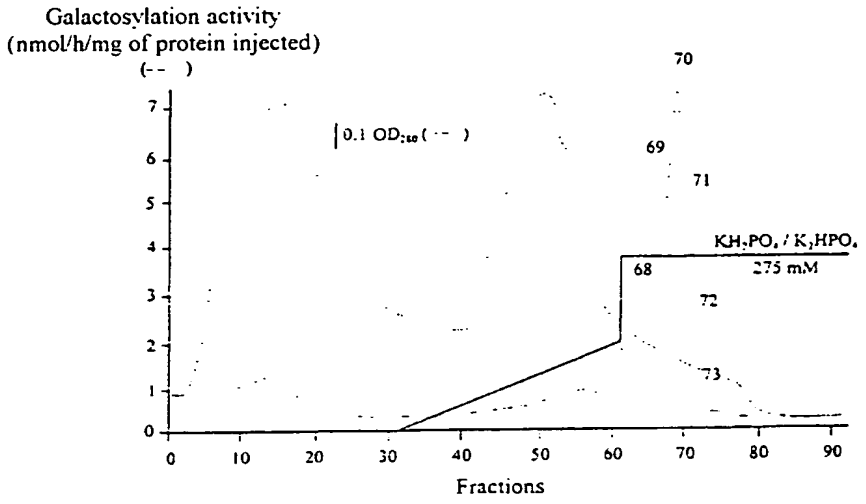


FIGURE 5A

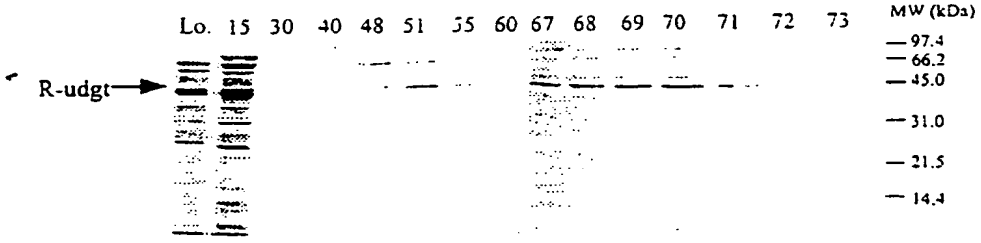


FIGURE 5B